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0500

TEAM 8

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/856,653

DATE: 07/18/97
TIME: 06:15:17

INPUT SET: S19057.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING        ENTERED
 2
 3   (1)     General Information
 4
 5           (i) APPLICANT: Russell, John
 6                          Colpitts, Tracey
 7
 8          (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
 9                   FOR DETECTING DISEASES OF THE PROSTATE
10
11         (iii) NUMBER OF SEQUENCES: 16
12
13          (iv) CORRESPONDENCE ADDRESS:                RECEIVED
14             (A) ADDRESSEE: Abbott Laboratories
15             (B) STREET: 100 Abbott Park Road          FEB 1998
16             (C) CITY: Abbott Park
17             (D) STATE: IL                             GRO 1800
18             (E) COUNTRY: USA
19             (F) ZIP: 60064-3500
20
21          (v) COMPUTER READABLE FORM:
22             (A) MEDIUM TYPE: Diskette
23             (B) COMPUTER: IBM Compatible
24             (C) OPERATING SYSTEM: DOS
25             (D) SOFTWARE: FastSEQ for Windows Version 2.0
26
27          (vi) CURRENT APPLICATION DATA:
28             (A) APPLICATION NUMBER:
29             (B) FILING DATE:
30             (C) CLASSIFICATION:
31
32         (vii) PRIOR APPLICATION DATA:
33             (A) APPLICATION NUMBER:
34             (B) FILING DATE:
35
36
37
38        (viii) ATTORNEY/AGENT INFORMATION:
39             (A) NAME: Becker, Cheryl L.
40             (B) REGISTRATION NUMBER: 35,441
41             (C) REFERENCE/DOCKET NUMBER: 6105.US.01
42
43          (ix) TELECOMMUNICATION INFORMATION:
44             (A) TELEPHONE: 847/937-6100
45             (B) TELEFAX: 847/938-2623
46             (C) TELEX:
```

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```
47
48               (2) INFORMATION FOR SEQ ID NO:1:
49
50          (i) SEQUENCE CHARACTERISTICS:
51             (A) LENGTH: 279 base pairs
52             (B) TYPE: nucleic acid
53             (C) STRANDEDNESS: single
54             (D) TOPOLOGY: linear
55
56
57          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59   CAGTGACCAT GAAGGCTGTG CTGCTTGCCC TGTTGATGGC AGGCTTGGCC CTGCAGCCAG      60
60   GCACTGCCCT GCTGTGCTAC TCCTGCAAAG CCCAGGTGAG CAACGAGGAC TGCCTGCAGG     120
61   TGGAGAACTG CACCCAGCTG GGGGAGCAGT GCTGGACCGC GCGCATCCGC GCAGTTGGCC     180
62   TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAACTGCGT GGATGACTCA CAGGACTACT     240
63   ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACT                           279
64
65               (2) INFORMATION FOR SEQ ID NO:2:
66
67          (i) SEQUENCE CHARACTERISTICS:
68             (A) LENGTH: 207 base pairs
69             (B) TYPE: nucleic acid
70             (C) STRANDEDNESS: single
71             (D) TOPOLOGY: linear
72
73
74          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
75
76   GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC      60
77   ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG     120
78   GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC     180
79   CTGACCGTCA TCAGCAAAGG CTGCAGC                                        207
80
81               (2) INFORMATION FOR SEQ ID NO:3:
82
83          (i) SEQUENCE CHARACTERISTICS:
84             (A) LENGTH: 265 base pairs
85             (B) TYPE: nucleic acid
86             (C) STRANDEDNESS: single
87             (D) TOPOLOGY: linear
88
89
90          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
91
92   CGAGGACTGC CTGCAGGTGG AGAACTGCAC CCAGCTGGGG GAGCAGTGCT GGACCGCGCG      60
93   CATCCGCGCA GTTGGCCTCC TGACCGTCAT CAGCAAAGGC TGCAGCTTGA ACTGCGTGGA     120
94   TGACTCACAG GACTACTACG TGGGCAAGAA GAACATCACG TGCTGTGACA CCGACTTGTG     180
95   CAACGCCAGC GGGGCCCATG CCCTGCAGCC GGCTGCCGCC ATCCTTGCGC TGCTCCCTGC     240
96   ACTCGGCCTG CTGCTCTGGG GACCC                                          265
97
98               (2) INFORMATION FOR SEQ ID NO:4:
99
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100                (i) SEQUENCE CHARACTERISTICS:
101                    (A) LENGTH: 196 base pairs
102                    (B) TYPE: nucleic acid
103                    (C) STRANDEDNESS: single
104                    (D) TOPOLOGY: linear
105
106
107                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
108
109      CTCGGCCTGC TGCTCTGGGG ACCCGGCCAG CTATAGGCTC TGGGGGGCCC CGCTGCAGCC    60
110      CACACTGGGT GTGGTGCCCC AGGCCTCTGT GCCACTCCTC ACAGACCTGG CCCAGTGGGA   120
111      GCCTGTCCTG GTTCCTGAGG CACATCCTAA CGCAAGTCTG ACCATGTATG TCTGCACCCC   180
112      TGTNCCCCAC CCTGAC                                                   196
113
114                (2) INFORMATION FOR SEQ ID NO:5:
115
116                (i) SEQUENCE CHARACTERISTICS:
117                    (A) LENGTH: 233 base pairs
118                    (B) TYPE: nucleic acid
119                    (C) STRANDEDNESS: single
120                    (D) TOPOLOGY: linear
121
122
123                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
124
125      CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT GAGGCACATC CTAACGCAAG TCTGACCATG    60
126      TATGTCTGCN CCCCTGTCCC CCACCCTGAC CCTCCCATGG CCCTCTCCAG GACTCCCACC   120
127      CGGCAGATCA GCTCTAGTGA CACAGATCCG CCTGCAGATG GCCCCTCCAA CCCTCTCTGC   180
128      TGCTGTTTCC ATGGCCCAGC ATTCTCCACC CTTAACCCTG TGCTCAGGCA CCT          233
129
130                (2) INFORMATION FOR SEQ ID NO:6:
131
132                (i) SEQUENCE CHARACTERISTICS:
133                    (A) LENGTH: 236 base pairs
134                    (B) TYPE: nucleic acid
135                    (C) STRANDEDNESS: single
136                    (D) TOPOLOGY: linear
137
138
139                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
140
141      CCCAGCATTC TCCACCCTTA ACCCTGTGCT CAGGCACCTC TTCCCCCAGG AAGCCTTCCC    60
142      TGCCCACCCC ATCTATGACT TGAGCCAGGT CTGGTCCGTG GTGTCCCCCG CACCCAGCAG   120
143      GGGACAGGCA CTCAGGAGGG CCCAGTAAAG GCTGAGATGA AGTGGACTGA GTAGAACTGG   180
144      AGGACAAGAG TCGACGTGAG TTCCTGGGAG TCTCCAGAGA TGGGGCCTGG AGGCCT        236
145
146                (2) INFORMATION FOR SEQ ID NO:7:
147
148                (i) SEQUENCE CHARACTERISTICS:
149                    (A) LENGTH: 122 base pairs
150                    (B) TYPE: nucleic acid
151                    (C) STRANDEDNESS: single
152                    (D) TOPOLOGY: linear
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```
153
154
155              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
156
157    CCTGGGAGTC TCCAGAGATG GGGCCTGGAG GCCTGGAGGA ANGGNANCAG GCCTCACATT      60
158    CGTGGGGCTC CCTGAATGGC AGCCTGAGCA CAGCGTAGGC CCTTAATAAA CACCTGTTGG     120
159    AT                                                                   122
160
161         (2) INFORMATION FOR SEQ ID NO:8:
162
163         (i) SEQUENCE CHARACTERISTICS:
164             (A) LENGTH: 968 base pairs
165             (B) TYPE: nucleic acid
166             (C) STRANDEDNESS: single
167             (D) TOPOLOGY: linear
168
169
170         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
171
172    CAGTGACCAT GAAGGCTGTG CTGCTTGCCC TGTTGATGGC AGGCTTGGCC CTGCAGCCAG      60
173    GCACTGCCCT GCTGTGCTAC TCCTGCAAAG CCCAGGTGAG CAACGAGGAC TGCCTGCAGG     120
174    TGGAGAACTG CACCCAGCTG GGGGAGCAGT GCTGGACCGC GCGCATCCGC GCAGTTGGCC     180
175    TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAACTGCGT GGATGACTCA CAGGACTACT     240
176    ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACTT GTGCAACGCC AGCGGGGCCC     300
177    ATGCCCTGCA GCCGGCTGCC GCCATCCTTG CGCTGCTCCC TGCACTCGGC CTGCTGCTCT     360
178    GGGGACCCGG CCAGCTATAG GCTCTGGGGG GCCCCGCTGC AGCCCACACT GGGTGTGGTG     420
179    CCCCAGGCCT CTGTGCCACT CCTCACAGAC CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT     480
180    GAGGCACATC CTAACGCAAG TCTGACCATG TATGTCTGCA CCCCTGTCCC CCACCCTGAC     540
181    CCTCCCATGG CCCTCTCCAG GACTCCCACC CGGCAGATCA GCTCTAGTGA CACAGATCCG     600
182    CCTGCAGATG GCCCCTCCAA CCCTCTCTGC TGCTGTTTCC ATGGCCCAGC ATTCTCCACC     660
183    CTTAACCCTG TGCTCAGGCA CCTCTTCCCC CAGGAAGCCT TCCCTGCCCA CCCCATCTAT     720
184    GACTTGAGCC AGGTCTGGTC CGTGGTGTCC CCCGCACCCA GCAGGGGACA GGCACTCAGG     780
185    AGGGCCCAGT AAAGGCTGAG ATGAAGTGGA CTGAGTAGAA CTGGAGGACA AGAGTCGACG     840
186    TGAGTTCCTG GGAGTCTCCA GAGATGGGGC CTGGAGGCCT GGAGGAANGG NANCAGGCCT     900
187    CACATTCGTG GGGCTCCCTG AATGGCAGCC TGAGCACAGC GTAGGCCCTT AATAAACACC     960
188    TGTTGGAT                                                             968
189
190         (2) INFORMATION FOR SEQ ID NO:9:
191
192         (i) SEQUENCE CHARACTERISTICS:
193             (A) LENGTH: 68 base pairs
194             (B) TYPE: nucleic acid
195             (C) STRANDEDNESS: single
196             (D) TOPOLOGY: linear
197
198         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
199
200    AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC      60
201    CGGGAATT                                                           4  68
202
203         (2) INFORMATION FOR SEQ ID NO:10:
204
205         (i) SEQUENCE CHARACTERISTICS:
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206	(A) LENGTH: 68 base pairs
207	(B) TYPE: nucleic acid
208	(C) STRANDEDNESS: single
209	(D) TOPOLOGY: linear
210	
211	
212	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
213	
214	AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG 60
215	GAATTCCG 68
216	
217	(2) INFORMATION FOR SEQ ID NO:11:
218	
219	(i) SEQUENCE CHARACTERISTICS:
220	(A) LENGTH: 123 amino acids
221	(B) TYPE: amino acid
222	(C) STRANDEDNESS: single
223	(D) TOPOLOGY: linear
224	
225	(ii) MOLECULE TYPE: None
226	
227	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
228	
229	Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
230	1 5 10 15
231	Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
232	20 25 30
233	Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
234	35 40 45
235	Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
236	50 55 60
237	Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
238	65 70 75 80
239	Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
240	85 90 95
241	Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
242	100 105 110
243	Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
244	115 120
245	
246	(2) INFORMATION FOR SEQ ID NO:12:
247	
248	(i) SEQUENCE CHARACTERISTICS:
249	(A) LENGTH: 34 amino acids
250	(B) TYPE: amino acid
251	(C) STRANDEDNESS: single
252	(D) TOPOLOGY: linear
253	
254	(ii) MOLECULE TYPE: None
255	
256	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
257	
258	Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn Glu Asp

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/856,653*

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Line	Error	Original Text